What is Claimed is:

1. A method for detecting a mutation, comprising:

a) amplifying a target polynucleotide using a forward primer and a reverse primer to produce an amplified target polynucleotide;

b) contacting said amplified target polynucleotide with two or more restriction endonucleases to generate at least one restriction fragment, said restriction fragment comprising two single-stranded fragments of 2-32 nucleotides each, wherein at least one of said single-stranded fragment contains a mutation sequence, said mutation sequence being a base substitution, deletion or insertion; and

c) measuring the molecular weights of said single-stranded fragments,

d) comparing said molecular weights of said single-stranded fragments to the molecular weights of control fragments,

wherein if said molecular weights of said single-stranded fragments differs from the molecular weights of said control fragments, said mutation is detected.

2. The method according to claim 1, wherein said restriction fragment comprising two single-stranded fragments includes one mutation among two or more different mutations in only one of said single stranded fragment and all other mutations in the other said single stranded fragment.

3. A method for detecting a mutation, comprising:

a) amplifying a target polynucleotide using a forward primer and a reverse primer to produce an amplified target polynucleotide;

b) cleaving the amplified target polynucleotide using a first restriction endonuclease and a second restriction endonuclease, under conditions in which

said second restriction endonuclease does not cleave said amplified target polynucleotide;

c) cleaving the product of step b) under conditions in which said second restriction endonuclease cleaves said amplified target polynucleotide to produce a plurality of restriction fragments that comprise single-stranded fragments;

d) measuring the molecular weight of said single-stranded fragments; and

e) comparing said molecular weights of said single-stranded fragments to the molecular weights of control fragments,

wherein if said molecular weights of said single-stranded fragments differs from the molecular weights of said control fragments, said mutation is detected..

4. The method according to claim 1, wherein said contacting is performed using restriction endonucleases having different optimum temperatures.

5. The method according to claim 3, wherein said first restriction endonuclease has a different optimum temperature than said second restriction endonuclease.

6. The method according to claim 4, wherein a first restriction endonuclease is selected from the group consisting of Fok1, Bbv I, Bsg I, Bcg I, Bpm I, BseR I and Bae I, and a second restriction enzyme is selected from the group consisting of BstF5 I, Taq I, BsaB I, Btr I, BstAP I, Fau I, Bcl I, Pci I and Apo I.

7. The method according to claim 5, wherein said first restriction endonuclease is selected from the group consisting of Fok1, Bbv I, Bsg I, Bcg I, Bpm I, BseR I and Bae I, and said second restriction endonuclease is selected from the group consisting of BstF5 I, Taq I, BsaB I, Btr I, BstAP I, Fau I, Bcl I, Pci I and Apo I.

8. The method according to claim 1, wherein said amplified target polynucleotide comprises a tyrosine-methionine-aspartate-aspartate (YMDD) site which is an active site of DNA polymerase of hepatitis B virus.

9. The method according to claim 3, wherein said amplified target polynucleotide comprises a tyrosine-methionine-aspartate-aspartate (YMDD) site which is an active site of DNA polymerase of hepatitis B virus.

10. The method according to claim 1, wherein said amplified target polynucleotide comprises a 5'-NCR (non-coding region) site of a hepatitis C virus.

11. The method according to claim 3, wherein said amplified target polynucleotide comprises 5'-NCR (non-coding region) site of a hepatitis C virus.

12. A primer for analyzing a gene mutation comprising a first primer binding sequence, a restriction enzyme recognition sequence and a second primer binding sequence, wherein a polynucleotide fragment that is amplified using said primer, and is cleaved by two or more restriction endonucleases that recognize said restriction enzyme recognition sequence, comprises a mutation sequence, and wherein the size of said fragment is from 2 to 32 nucleotides in length.

13. The primer according to claim 12, wherein said primer is a forward primer and is selected from the group consisting of SEQ ID NO: 2, 7, 12, 20, 25 and 30.

14. The primer according to claim 12, wherein said two or more restriction endonucleases have different optimum temperatures.

15. The primer according to claim 14, wherein a first restriction endonuclease is selected from the group consisting of Fok1, Bbv I, Bsg I, Bcg I, Bpm I, BseR I and Bae I, and a second restriction enzyme is selected from the group consisting of BstF5 I, Taq I, BsaB I, Btr I, BstAP I, Fau I, Bcl I, Pci I and Apo I.

16. The primer according to claim 12, wherein said primer is used for mutation analysis of the 2741st or 3597th base site of the 4th intron of human maspin gene or for mutation analysis of lamivudine resistant hepatitis B virus or hepatitis C virus.